LXR Agonist Compound A Activates the Expression of SSE

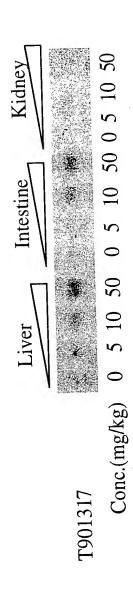
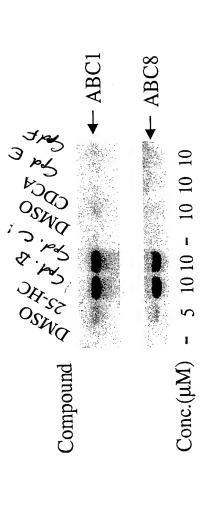


FIGURE 1

Oxysterol and LXR Agonists Activate the Expression of Cholesterol Transporters, ABC1 and ABC8

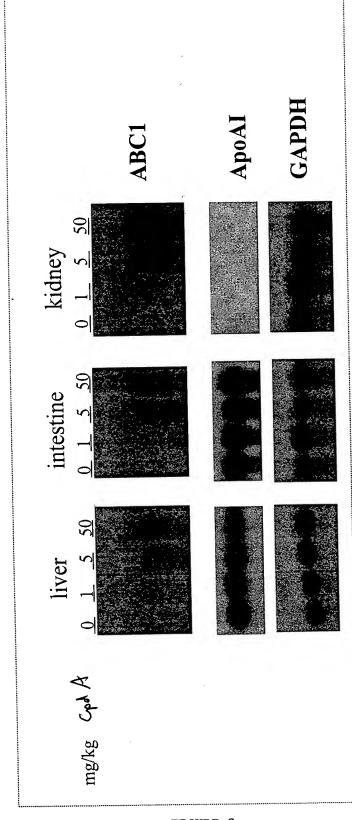


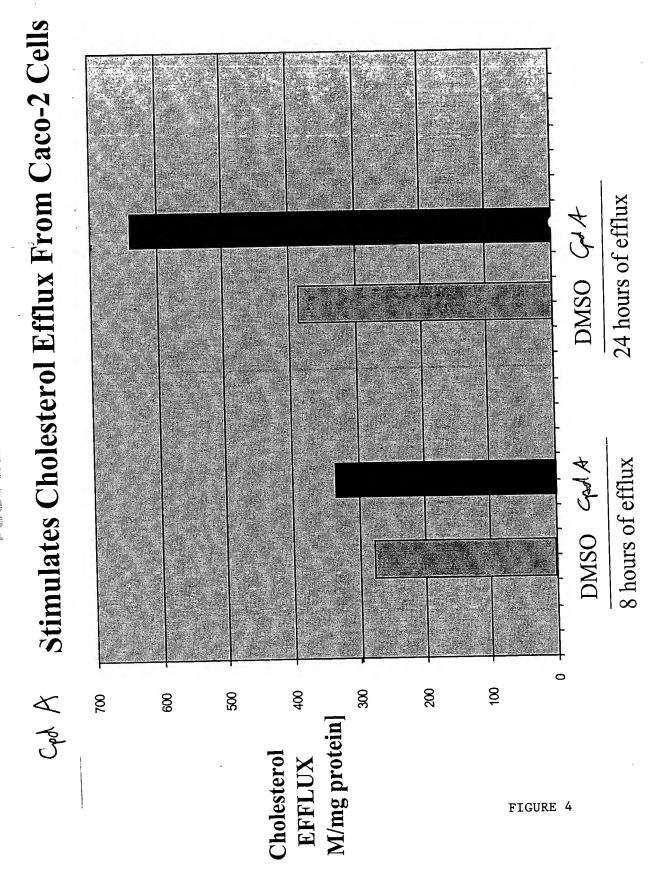
LXR agonist: 'God B, C

FXR agonist: Cpd E, F

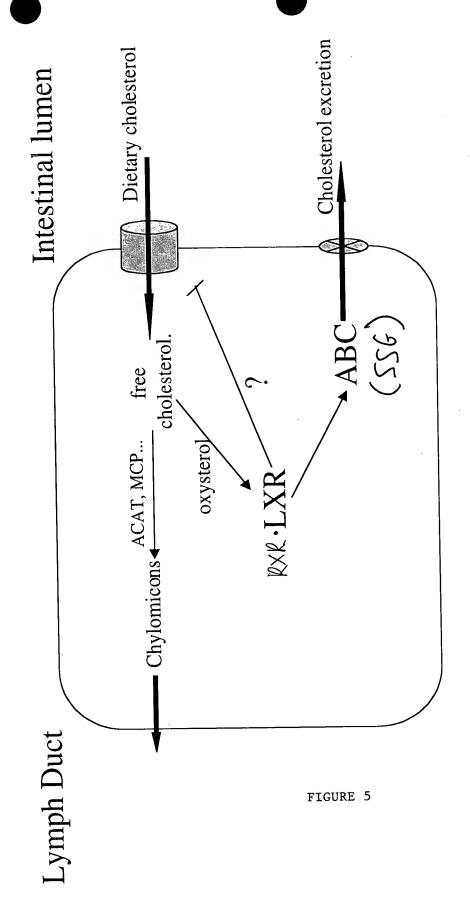
FIGURE 2

Induction of ABC1 in Liver, Intestine and Kidney of C57BL/6 Mice by LXRa Agonist God A





How Does LXR Regulate Cholesterol Absorption? -A Working Model -



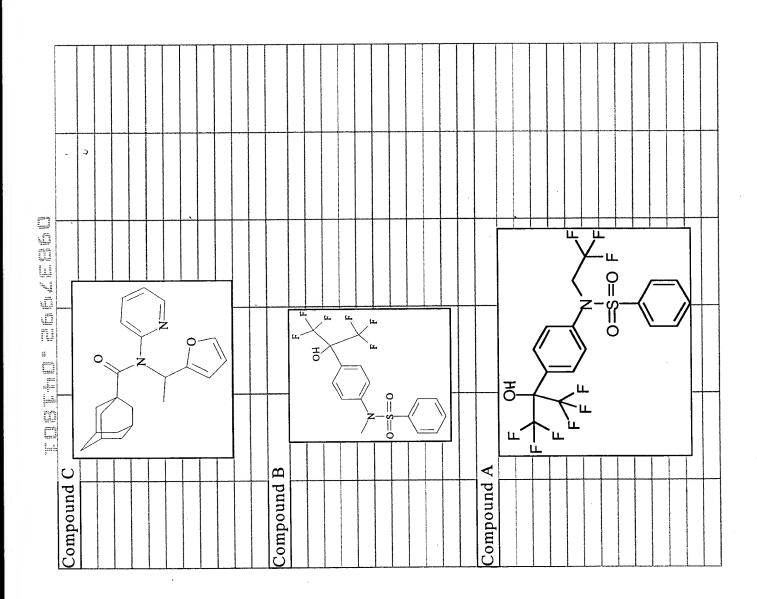


FIGURE 6

;

GGENCYCCTCAGCATCTCTGGGGTTTATTGGGATTTATCAGAAAAGCCATACCATTCCTTTAAAAATCCTGGGTTATTTACATTCCAAAAAATGCTGTTGTGGGATTCTGGGGTTTTTACGGCCTGAA A L L S I S G L L I G S G F I R N I Q E M P I P L K I L G Y F T F Q K Y C C E I L V V N E F Y G L N> V C Y W T L G L Y P E V A R F G Y F S A A L L A P H L I G E F L T L V L L G I V Q N P N I V N S I V> N N C G Y P C P E H S N P F D F Y M D L T S V D T Q S R E R E I E T Y K R V Q M L E C A F K E S D I> CIATCACAAAATTCTGGAGAACATTGAAAGCACGATACCTTACCCATGGTTCCTTTCAAAACAAAAGATCCTCGGGAAGCAGGTGCCTGGGGAGGAGGAGGAGAAAAACTTAATGAGGAATAAGCA Y H K I L E N I E R A R Y L K T L P M V P F K T K D P P G M F G K L G V L L R R V T R N L M R N K Q> TGIGIGITATIGGACITCIGGGCITGIAICCIGAAGITGCCAGAITIGGATAITITCICCCCCCTCTTTTTGGACAATTTTCTAACACTTGTGCTGGTATAGTCCAAAACCCTAATAITGTCAACAGTATAGT SDVFLSSLTVRETLRYTAMLALCRSSADFYNKKVEAVMTELSLSHVADQM> CAATAACTETGSTTACCCCTGTCCTGAACATTCCAATGCTTTTTTACATGGACTTGACATCGGACACCCAAAGCAGGAGAGCGGGAAATAGAAACGTACAAGAGATGCTGGAATGTGCCTTCAAGGAATCTGACAT MGELPFLSPEGARGPHINRGSLSSLEQGSVTGTEA> GAGCGAOGTITITICTGAGCAGCCTCACTIGTGCGAGACGTTGCGATACACAGCGATGCTGGCCCTCTGCCGCGGACTTCTACAACAAGAAGGTAGAGGCAGTCATGACAGGCTGAGCCTGAGCCACGTGGGCGGAACTAAT M L N A V N L F P M L R A V S D Q E S Q D G L Y H K W Q M L L A Y V L H V L P F S V I A T V I F S GGGACAGSCCACTAGAAAATTCACTTGCCATTGCCTAGCCATGGGTGACCTCTCTTCTGAGTCCAGAGGGAGCCAGAGGGGCCTCACATCAACAGAGGÁCTCTGAGCTCCCTGGAGCTAGGGTTCGGTCACGGGCAAAAAGC

GETCATCCTAGGAATAGTGATTTTTAAAGTCAGGGACTACCTGATTAGCAGTAAGAGTGAAGGGGTTAATGGGCACGCCCCACTGTGGAGCACTGTCTTCAACCATCAGÀTTCCATCTGCGAC VILGIV IF KVRDYLIS XX>

TACATICCAAAAATATIGCAGIGAGATICTIGTAGICAATGAGTICTACGGACTGAATITICACTTGTGGCACTGACGAACTGGTGACAAACTGCAAGAAATTGATGAGAAATTGATGAGAAAACCTGCCCAGG T F Q K Y C S E I L V V N E F Y G L N F T C G S S N V S V T T N P M C A F T Q G I Q F I E K T C P G> S K L G V L L R R V T R N L V R N K L A V I T R L L Q N L I M G L F L L F F V L R V R S N V L K G A> I O D R V G L L Y Q F V G A T P Y T G M L N A V N L F P V L R A V S D Q E S Q D G L Y Q K W Q M M L> AYALHVLPFSVVATMIFSSVCYWTLGLHPEVARFGYFSAALLAPHLIGEF> I E T S K R V Q M I E S A Y K K S A I C H K T L K N I E R M K H L K T L P M V P F K T K D S P G V F> K K V E A V M A E L S L S H V A D R L I G N Y S L G G I S T G E R R R V S I A A Q L L Q D P K V M L> GITTGATGAGCCAACCACAGGCCTGGACTAGCTAATGAGATTGTCGTCCTGGTGGAACTGGCTGCGAATTGTGGTTCTCACCATTCACCAGCCCGTTCTGAGCTTTTTCAGCTCTTTGAGAAAATTGCCAT FDEPTTG LDCMTANQIOVLL VLLVELARRN 1VVLT THQPRSELF LARNN 1 VVLT IHQPRSELFQLFDKIAIS 1650 M G D L S S L T P G G S M G L> R Q I L K D V S L Y V E S G Q I M C I L G S S G S G K T T L L D A M S G R L G R A G T F L G E V Y V> N G R A L R R E Q F Q D C F S Y V L Q S D T L L S S L T V R E T L H Y T A L L A I R R G N P G S F Q> AATAGAAACCICCAAGAGGCCAGATGAATGTGCCCTACAAGAAATCAGCAATTTGTCATAAAACTTTGAAGAATATGAAAGAATGAAAACATGATACCTAACAATGGTTCCTTTCAAAACCTAGAAGTTCTCCTGGAGTTTT 1350 GAAGAGGCCGTCATGGCAGACTGAGTCTGAGCCATGTGGCAACTGATTGGCAACTACAGCGTTGGGGGGCATTTCCACGGGTGAGCGGCCGGGTCTCCATGGCAGCCCAGCTGCTCCAGGATCCTAAGGTCATGCT 1875 1275 675

FIGURE 8

tigctcttacaactitgcagggacatgtggttatttggaaatttgtggccgagcggacccaagaatgtaaaataatattcataaacctatggg

Alignment of Human and Mouse SSG Protein Sequences

hSSG.pro	MGDLSSLTPG GSMGLQVNRG SQSSLEGAPA TAPEP-HSLG ILHASYSVSH	49
mSSG.pro	MGELPFLSPE GARGPHINRG SLSSLEQGSV TGTEARHSLG VLHVSYSVSN	50
hSSG.pro	RVRPWWDITS CROOWTROIL KDVSLYVESG QIMCILGSSG SGKTTLLDAM	99
mSSG.pro	RVGPWWNIKS COOKWDROIL KDVSLYIESG QIMCILGSSG SGKTTLLDAI	100
hSSG.pro	SGRLGRAGTF LGEVYVNGRA LRREQFQDCF SYVLQSDTLL SSLTVRETLH	149
mSSG.pro	SGRLRRTGTL EGEVFVNGCE LRRDQFQDCF SYVLQSDVFL SSLTVRETLR	150
hSSG.pro	YTALLAIRRG NPGSFOKKVE AVMAELSLSH VADRLIGNYS LGGISTGERR	199
mSSG.pro	YTAMLALCRS SADFYNKKVE AVMTELSLSH VADQMIGSYN FGGISSGERR	200
hSSG.pro	RVSTAAQLLQ DPKVMLFDEP TTGLDCMTAN QIVVLLVELA RRNRIVVLTI	249
mSSG.pro	RVSTAAQLLQ DPKVMMLDEP TTGLDCMTAN QIVLLIAELA RRDRIVIVTI	250
hSSG.pro	HOPRSELFOL FOKIAILSFG ELIFCGTPAE MEDFFNDCGY PCPEHSNPFD	299
mSSG.pro	HOPRSELFOH FOKIAILTYG ELVFCGTPEE MEGFFNNCGY PCPEHSNPFD	300
hSSG.pro	FYMDLTSVDT QSKEREIETS KRVQMIESAY KKSAICHKTL KNIERMKHLK	349
mSSG.pro	FYMDLTSVDT QSREREIETY KRVQMLECAF KESDIYHKIL ENIERARYLK	350
hSSG.pro	TLPMVPFKTK DSPGVFSKLG VLLRRVTRNL VRNKLAVITR LLQNLIMGLF	399
mSSG.pro	TLPMVPFKTK DPPGMFGKLG VLLRRVTRNL MRNKQAVIMR LVQNLIMGLF	400
hSSG.pro	LLEFVLRVRS NVLKGAIQDR VGLLYQFVGA TPYTCMLNAV NLFPVLRAVS	449
mSSG.pro	LIFYLLRVQN NTLKGAVQDR VGLLYQLVGA TPYTCMLNAV NLFPMLRAVS	450
hSSG.pro	DQESQDGLYQ KWQMMLAYAL HVLPFSVVAT MIFSSVCYWT LGLHPEVARF	499
mSSG.pro	DQESQDGLYH KWQMLLAYVL HVLPFSVIAT VIFSSVCYWT LGLYPEVARF	500
hSSG.pro	GYFSAALLAP HLIGEFLTLV LLGIVONPNI VNSVVALLSI AGVEVGSGFL	549
mSSG.pro	GYFSAALLAP HLIGEFLTLV LLGIVONPNI VNSIVALLSI SGLLIGSGFI	550
hSSG.pro	RNIQEMPIPF KIISYFTFOK YCSEILVVNE FYGLNFTCGS SNVSVITNPM	599
mSSG.pro	RNIQEMPIPL KILGYFTFOK YCCEILVVNE FYGLNFTCGG SNTSMLNHPM	600
hSSG.pro	CAFTOGIOFI EKTCPGATSR FIMNFLILYS FIPALVILGI VVFKIRDHLI	649
mSSG.pro	CAITOGVOFI EKTCPGATSR FTANFLILYG FIPALVILGI VIFKVRDYLI	650
hSSG.pro	SR	651
mSSG.pro	SR	652

Reference Number: 6711 Stanford RH Panel: TNG4 Lowest LOD Reported: 6 Chromosome Value: 0

Results for HT

Submitted

001000000000001000100

SHGCNAME CHROM# LOD_SCORE DIST.(cRs)

1 SHGC-36672 2 7.52 35 001000000000R0100Q100

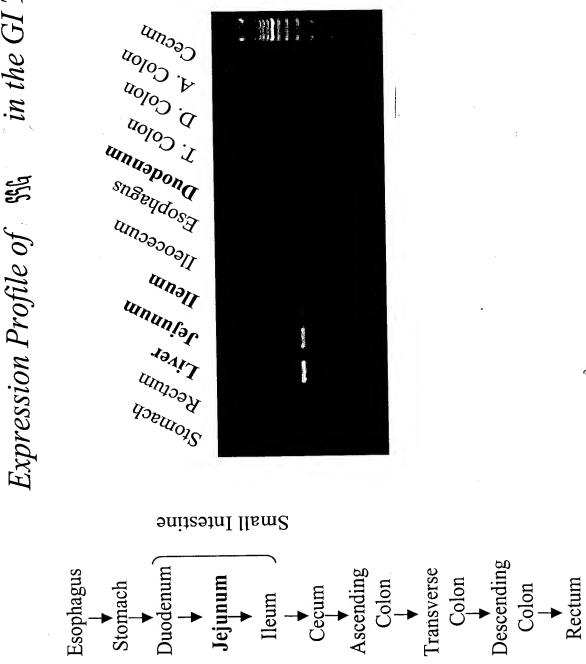
001000000000101000100

3 SHGC-699 2 6.03 48 9 000000100000011000100

The number of markers searched was 32440.

FIGURE 10

in the GI Tract



LICHE II

is Predominantly Expressed in the Liver and Small Intestine 25.5 Human

shundy 7_{estis} u_{aalds} S. Intestine Prostate 78_d N_{ENO} CO/02 S. Muscle placenta p b^{gUCLGG8} Brain Heart Kidney

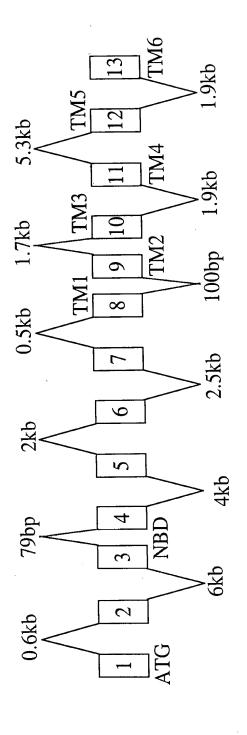
is Selectively Expressed in the Liver and Small Intestine Mouse !

S. Intestine Sind S. Intestine Spleen Liver Spleen Liver Brain Thymus S. Muscle Jestis Skin

Mouse Multiple Tissue RT-PCR

cDNA Cloning and Genomic Organization of 𝔥ﮔੈੈੈ।

- The predicted human and mouse proteins share 80% identity and is 28% identical to Drosophila Brown
- Human ABCG5 contains 13 exons and spans at least 25kb of genomic DNA



Human SSG nucleotide sequence—13 Exons

Exon 1 GTCAGGTGGAGCAGGCAGTCTGCCACGGGCTCCCCAACTGAAGCCACTCTGGGGA GGGTCCGGCCACCAGAAAATTTGCCCAGCTTTGCTGCCTGTTGGCCATGGGTGACCTCTC ATCTTTGACCCCCGGAGGGTCCATGGGTCTCCAAGTAAACAGAGGCTCCCAGAGCTCCCT TGCCACCGCCCCGGAGCCTCACAGCCTGGGCATCCTCCATGCCTCCTA CAC<mark>T</mark>CÃČCGCGTGAGGCCCTGGTGGGACATCACATCTTGCCGGCAGCAGTGGAC CAGGCAGATCCTCAAAGATGTCTCCTTGTACGTGGAGAGCGGGCAGATCATGTGCATCCT GGGAAAACCACGCTGCTGGACGCCATGTCCGGGAGGCTGGGGCG GGTGTATGTGAACGGCCGGGCGCTGCGCCGGGAGCAGTT PACACCGCGCTGCTGGCCATCCGCCGCGGCAATCCCGGCTCCTTCCA $oldsymbol{\mathfrak{h}}$ CATGGCAGAGCTGAGTCTGAGCCATGTGGCAGACCGACTGAT ATTTCCACGGGTGAGCGGCGCCGGGTCTCCATCGCAGC TAAĞĞTCATGCTGTTTGATGAGCCAACCACAGGCCTGGACTG CATGACTGCTAATCAGATTGTCGTCCTCCTGGTGGAACTGGC CCTGAGCTTCGGAGAGCTGATTTTCTGTGGCACGCCAGCGGA TGACTGCGGTTACCCTTGTCCTGAACATTCAAACCCTTTTGACTTCTATATĞĞÄCCTGAC GTCAGTGGATACCCAAAGCAAGGAACGGGAAATAGAAACCTCCAAGAGAGTCCAGATGAT AGAATCTGCCTACAAGAAATCAGCAATTTGTCATAAAACTTTGAAGAATATTGAAAGAAT GAAACACCTGAAAACGTTACCAATGGTTCCTTTCAAAACCAAAGATTCTCCTGGAGTTTT CTCTAAACTGGGTGTTCTCCTGAGGAGGTGACAAGAAACTTGGTGAGAAATAAGCTGGC AGTGATTACGCGTCTCCTTCAGAATCTGATCATGGGTTTGTTCCTCCTTTTCTTCGTTCT GCGGGTCCGAAGCAATGTGCTAAAGGGTGCTATCCAGGACCGC GTTTGTGGGCGCCACCCCGTACACAGGCATGCTGAACGCTGTGAATCTGTTTCČČČĞTGCT GCGAGCTGTCAGCGACCAGGAGAGTCAGGACGGCCTCTACCAGAAGTGGCAGATGATGCT TCCCCTTCAGCGTTGTTGCCACCATGATTTTCAGCAGTGT TGGGCTTACATCCTGAGGTTGCCCGATTTGGATATTTTTCTGCTGC TCTCTTGGCCCCCCACTTAATTGGTGAATTTCTAACTCTTGTGCTACTTGGTATCGTCCA AAATCCAAATATAGTCAACAGTGTAGTGGCTCTGCTGCTCCATTGCGGGGGTGCTTGTTGG ATCTGGATTCCTCAGAÃÃCATACAAGAAATGCCCATTCCTTTTAAAATCATCAGTTATTT TACATTCCAAAAATATTGCAGTGAGATTCTTGTAGTCAATGAGTTCTACGGACTGAATTT CACTTGTGCAGCTCAAATGTTTCTGTGACAACTAATCCAATGTGTGCCTTCACTCAAGG AATTCAATTCATTGAGAAAACCTGCCCAGGTGCAACATCTAGATTCACAATGAACTTTCT

Exon number	exon size	5' splicing site	3' splicing site	Intron size
1 ·			GCGTCAGgtaaggcag	~600bp
2	124	cctttaaagCCACCGC	AGCTCAGgtaagcttg	~6kb
3	137	gcccgcagGCTCCGG	CCTGCAGgtgggcgcg	79bp
4	103	ctcctgcagAGCGACA	AAGGTGGgtgcagccc	~4kb
5	129	tgcaggtggAGGCCGT	GATCCTAgtaagtggc	~2kb
6	140	tgctggcagAGGTCAT	TTTTCAGgtaagaggt	~2.5kb
7	130	tctggtcagCTCTTTG	TTCTATAgtaagtttt	~0.5kb
8	214	aacttttagTGGACCT	TCCTGAGgtaagaggc	100bp
9	206	tgttttcagGAGAGTG	AATCTGTgtaagtgcc	~1.7kb
10	139	catccccagTTCCCGT	GCTACTGgtgaggggtt	~1.9kb
11	186	cttttctagGACGCTG	TCCTCAGgtaagatat	~5.3kb
12	113	tttcttaagAAACATA	ACTTGTGgtaagtatt	~1.2kb
13		ccttgacagGCAGCTC		
Total				~25.9kb

Exonic sequences in capital letter

FIGURE 14B (2 of 2)